2 Spitting image: decode me!

> **spitting image, spit 'n' image.** *Informal*. exact likeness; . . . bef. 950; (v.) ME *spitten,* OE *spittan;* c. G (dial.) *spitzen* to spit; akin to OE *spætan* to spit, *spætl* spittle . . .
>
> Dictionary.com, 2009[1]

In 2008, the California-based project 23andMe – a project that offers to estimate a person's predisposition to a number of traits and diseases on the basis of a saliva test – held a "spit party" during New York fashion week; volunteers would spit into a test tube to provide their DNA for sequencing and analysis. This was reported as a vibrant scene, a young couple opening their kits and donating saliva, to explore what their genomic constitution might tell them about their identity and the kind of life they might lead. Apparently, they were publicly celebrating both their self and their genome, staging their persona and their bodily essence for the media, in the process of lobbying for personal genomics and the company responsible for 23andMe, an affiliate of Google. An article in the *New York Times* announced the launch event by saying that 23andMe "wants people to think of their genomes as a basis for social networking," adding that "the company . . . hopes to make spitting into a test tube as stylish as ordering a ginger martini" (Salkin 2008). In November 2008, *Time Magazine* declared the retail DNA test of 23andMe the best innovation of the year. The year before, Apple's iPhone was the winner. Several other companies have started one form or another of retail genomics. This is consuming genomics, a rapidly growing business receiving both substantial financial support and intense public attention. Clearly, something new was in the air.

The notion of spitting and related concepts has proved to be a powerful metaphor. Exploring its social history is like following the trajectories of ancient DNA. The English verb to "spit" – to "spew" or to "expel saliva" – is of early medieval origin. The noun "spit," in the sense of "the very likeness," is more recent, attested from 1602, while "spitting image"

[1] Dictionary.com, 2009, http://dictionary.reference.com/browse/spitting. Accessed May 29.

is a twentieth-century thing, apparently from as early as 1901. It may be interesting to note that there has been some debate on the etymology of the phrase. Some have suggested it is derived from "*splitting* image," based on the two identical parts of a split plank of wood. Such an account would resonate perfectly with the modern concept of the double helix and the splitting of DNA, underlining the relevance of the idea of the "spitting image" for both modern gene talk and the genealogical tree. The discovery of the structure of DNA material has been heralded as the key to the understanding of the continuity and change of organisms and life forms, as the missing conceptual link of evolutionary theory finally solving the mystery of the "tree of life." Also, "splitting" might highlight the Western notion of the duality of the individual as a natural body and a social person, a notion often challenged nowadays by the monistic concept of the biosocial. Given such reasoning, the 23andMe spit party might just as well have been called a "split party." It seems, however, that the reference to spitting was based on "spit," not "split," an allusion to someone who is so similar to another as to appear to have been spat out of his or her mouth (Martin 2009).

The spit party and the notion of spitting image invite interesting anthropological questions: What are the overall spin-offs from personal genomics, especially with respect to the understanding of self, personhood, relationships, and ancestry? Despite sustained criticisms of the gene talk current in the West and the determinisms it implies, personal genomics along the lines of 23andMe seems to have a substantial public appeal. At the same time, the services offered by genomics companies give rise to new kinds of relations and networks based on genetic signatures presumed to be encoded in DNA. Like many others, I decided to indulge in a kind of spitting, mixing ethnographic observation, theoretical reflection, and narcissistic pleasure. One of the key companies in the development of personal genomics, deCODE genetics, happened to be located on the outskirts of my campus in Reykjavik, Iceland – within spitting distance, if you like.

Anthropology has played an important role in both personal genomics and studies of human variation, drawing on and expanding anthropological understanding of human genomes and their differences. I shall argue that in the process anthropology has coproduced new biosocial networks of associations along with a whole series of technologies and agencies engaged with biomedical research (Lock and Nguyen 2010). At the same time, the boundary between experts and laypersons has been blurred and refashioned. Projects such as 23andMe, deCODEme, Pathway Genomics, and Navigenics offer test kits for a low price (ranging from $250 to $2,500) – within the reach of the public, not just the research elite and the wealthy. Analyses and interpretations of genome scans are now a matter of intense public discussion through all kinds of media, including Web browsers and blog sites.

I would argue that up to a point, personal genomics has democratized genomic discourse. However, I also suggest that it is essential to attend to the biosocial relations of production involved, the potential hierarchies in the making in the assembly of personal genomics material and information through which consumers become active collaborators. The new genetics has not only called for the notion of the biosocial, advances in biomedicine and bioscience also make it pertinent to address the broad context of biosocial relations and labor processes (Dickenson 2007).

2.1 From physical anthropology to molecular anthropology

One useful avenue into early twentieth-century physical anthropology is the work of Ernest Albert Hooton at Harvard University. While his views were somewhat difficult to specify – he criticized Nazi physical anthropology, but at the same time he sponsored racist projects (see Marks 2008: 244) – he was one of the most prominent physical anthropologists in America. His work *Up from the Ape*, originally published in 1931, emphasized the continuity of human reasoning on anatomical difference.

> Actually, science is forced to recognize the differences in physical characteristics between the great divisions of mankind... For, the ordinary layman – the plain, untutored Homo sapiens – today and for the past thousands of years has observed these gross anatomical differences between the principal groups of this kind, has drawn the generally correct inference that they are transmitted from parents to children, and has attributed to them enormous political, sociological, psychological, and biological significance, rightly or wrongly. (Hooton 1946: 440–441)

While Hooton emphasized the antiquity of the theme of variability, he was eager to establish the autonomy of his scientific discipline with respect to the ignorant public. Commenting on race, he suggested that "confusions of usage are usually confined to the non-anthropological writing public. All anthropologists agree that the criteria of race are physical characteristics" (Hooton 1946: 447). At the same time, Hooton was keen to set his kind of science apart, irritated by challenges from social scientists.

> Man is an inveterate amateur of the taxonomy of his own kind. He cannot be argued out of the habit of connecting the physical differences he sees in individuals or groups with their equally obvious variations in behavior by any set of "social scientists," however loudly and persistently they tell him that there is no difference between black and white skins apart from exposure to the sun, and no difference between the psychology of a Mongolian and a White, apart from their having grown up in the Rice Bowl and the Dust Bowl, respectively. (Hooton 1946: 447)

For Hooton, skeletal material was the main source of information on human variability. The measurement and classification of bones became an obsession.

This is underlined by the extensive cross-cultural bone collections of the Peabody Museum at Harvard University, a kind of ethnographic atlas engraved in human bones. One of the students at Harvard, the Canadian-Icelandic anthropologist-explorer Vilhjalmur Stefansson, who contributed to the Peabody collection with a sample of medieval Icelanders, later did extensive ethnographic fieldwork among Canadian Inuit (between 1907 and 1918). A frequent phrase in his notebooks is "measured a few heads today" (Palsson 2005: 134, 204). Stefansson would move from one Inuit camp to another, lining up his "noble savages" to have them photographed and measured, setting up what he might have called measurement parties, precursors to the spit parties of 23andMe.

While the measurements of the bone people were exceedingly detailed, their classificatory scheme was highly simplistic and archaic, often with an implicit racial tone. Inevitably, the arrival of human genetics and biological anthropology after World War II provided a new avenue into the understanding of human variability, moving the kinds of measurements and classifications of skeletal material typically practiced by physical anthropologists during the first half of the twentieth century to the sidelines. Did they represent new paradigmatic "thought styles," in Fleck's sense? How radical were the breaks represented by the discovery of the double helix, the mapping of the human genome, the IT revolution and the Internet, the new economy, and related events and developments? Are we able to meaningfully situate ourselves and to domesticate our biases? Interestingly, given the context of skeletal analyses, one of the key illustrations in Fleck's book, originally published in 1935, demonstrates the usefulness of his thought-style perspective through discussion of changing understandings of human anatomy. "To obtain an even clearer picture of how scientific observation differs when two different thought styles are involved," he suggests, "it is perhaps appropriate to compare anatomical descriptions and illustrations in early and recent text books" (Fleck 1979: 133).

As Glick (2008: 240) remarks, the "great debate over race passed the Darwinian divide with scarcely an acknowledgment that anything had changed. Race was an issue marked by lack of ontological control, and that control would be gained slowly and with continuing conceptual difficulty until 'population thinking' introduced some clarity after World War II." The anthropological terrain of human variability in the wake of the new genetics, however, proved to be highly differentiated and rapidly changing, with both radical innovations in methods and perspectives and surprising continuities. Sommer (2008) emphasizes successive contests, following the birth of what Zuckerkandl identified as "molecular anthropology," over what counts as a legitimate epistemic object and authoritative information in the reconstruction of hominid evolution and human variation. The early molecular

anthropologists became convinced of the intrinsic superiority and mathematical precision of direct molecular data in comparison with the subjectivity of readings of anatomic data and the fossil record. For instance, at Berkeley, Washburn "heralded the new technologies as finally providing some scientific base to claims about human evolution," ridiculing "comparative anatomy as a kind of pseudo-science that had given rise to just-so stories" (Sommer 2008: 502). Over time, it was assumed, molecular studies would reduce if not eliminate the endemic bias involved when a species was studying itself informed by the belief in human exception. Ironically, however, in due course the analysts became overwhelmed by their faith in their methods. Vincent Sarich, for instance, one of those Washburn recruited at Berkeley, eventually argued against the mantra of "direct evidence" on the basis of molecular data, suggesting that "one no longer has the option of considering a fossil specimen older than about eight million years a hominid *no matter how it looks like*" (cited in Sommer 2008: 504; emphasis added). The thought style of molecular studies had become hegemonic, avoiding contradictory evidence.

2.2 Personal genomics, via Oxford and Reykjavik

The archaeology of the kind of personal genomics we now have on the horizon has several layers, among them maps of human genome diversity, population biobanks, digital genealogies, and the Internet. One of the pioneers of the genetics of ancestry and its commercialization through the Internet is Bryan Sykes of Oxford University, a human geneticist who founded the genetics testing firm Oxford Ancestors, probably the first service of its kind. His company offers people an opportunity to see which "clan" they belong to, tracing their ancestry to one of the seven daughters of Eve (Sykes 2001). To attract customers, Sykes (2001: 197) dramatizes the saga of the seven daughters: "What were they like, these women to whom almost everyone in Europe is connected by an unbroken, almost umbilical thread reaching back into the deep past?" For him, the power of DNA consists in the "token or a symbol of the shared ancestry it reveals rather than the body chemistry it directly controls" (Sykes 2001: 290). Common membership in a clan establishes a profound connection: "We look at each other and sense our deep umbilical connection . . . I feel we have *something very deep* in common" (Sykes 2001: 289; emphasis added).

One of the interesting sites of biomedical experimenting and personal genomics over the past decade is Iceland. Here as elsewhere, the introduction of human genetics represented a change in thought style, with new players and perspectives. Soon after World War II, physical anthropology developed at the University of Iceland through the work of Jón Steffensen, professor of medicine, and Jens Ó.P. Pálsson (no relation to me), founder of the Institute of

Anthropology (see, for example, Pálsson 1976). Both of them worked on skeletal material. Their interests, however, differed significantly (Palsson and Guðbjörnsson 2011); Steffensen emphasized medical and cultural issues without any hint at racial issues, whereas Pálsson tended to draw on public discourses on racial differences and "Nordic" people.

Jens Ó.P. Pálsson partly studied in Germany, where he became affiliated with the Mainz Institute of Anthropology. In Mainz he not only found a place for his fascination with racial types but also received financial support. In particular, he was supported by Ilse Schwidetzky, head of the institute, who was keen to get access to Icelandic data. Despite skillful lobbying in Iceland, decades of data collection, teams of collaborators, and considerable national and international funding, Pálsson's legacy remains small. Thus, he never taught or mentored anybody to speak of. Also, his publication record was meager. Moreover, his text was devoid of theory, focusing on classification and catalogs in the fashion of German physical anthropology, particularly the Breslauer or Breslauer/Mainzer Schule (Preuß 2009: 129). Perhaps he felt at the end of his career, at a time of rapid advances in human genetics, that his work was rather suddenly out of touch, a thought style that failed to sustain attention. Perhaps, too, he had also come to realize that the close connections to Schwidetzky and her entourage at Mainz, a branch of anthropology that remained publicly implicated with the Nazi past, isolated him both internationally and at home. Schwidetzky's anthropology was firmly grounded in the measurements of the Breslauer/Mainzer Schule and the racial typology of Egon Freiherr von Eickstedts, the leading racial theorist of Nazi Germany (see Preuß 2009: 132–134).

The deCODE projects draw on the development of flexible interdisciplinary research teams, powerful genomic laboratories, bioinformatics frameworks, and digital genealogies (Palsson 2007), all of which were involved in the making of deCODEme. The project was able to draw on several kinds of assets – in particular, large-scale efforts over several years to discover the genetic factors involved in common diseases and extensive genomic anthropological work on human populations and their migrations, ancestry, and mixing. All of this was important for developing the analyses and interactive frameworks offered by deCODEme. For a few years, the project offered both a "complete" scan ($2,000) and two narrower scans focusing on specific conditions – cancer ($500) and cardiovascular problems ($500) – but its services have now been discontinued.

2.3 deCODEme: a somewhat personal guided tour

I signed up for the complete scan, curious to find out how anthropological expertise was implicated in the project, to explore the analyses it offers, and to

see what the scan might tell me about myself and my roots. Two weeks after I sent my cheek swabs and the relevant forms, I received an e-mail from the company. The results were now available, and I would be able to access them through the password provided. For a few years, I regularly received messages from the company alerting me to both updated and new conditions and to further analyses of traits and health risks. Once I logged on to see the results, I was urged to "have fun browsing [my] ... genome," "dig into [my] ... DNA," explore my ancestry and my "genetic risks," play with maps and other visuals, search for specific genetic variants (SNPs or "snips"), and download my genotypes for 1.2 million SNPs (a 33-Mb data file).

The search for ancestry had six key features. The first, the "atlas," provided a comparison of one's genetic code with that of people from all over the world based on several hundred thousand genetic variants and more than a thousand reference individuals from fifty different populations worldwide. The atlas compared my genome with reference populations throughout the world, ranking regional clusters (1 to 6) in terms of their relevance to me, in order of genetic similarity: Europe (1), Southwest Asia (2), East Asia (3), America (4), Oceania (5), and Africa (6). In each case, I could zoom in on the population involved.

My genome, not surprisingly, turned out to have most in common with European reference groups (a genetic similarity of 83.99 percent), in particular those of Iceland, the Orkney Islands, France, and Russia. More astonishingly, the second feature, "ancestral origins," indicated that judging from chromosomes 1–22, my ancestry is no less than 7 percent East Asian, 16 percent according to the X chromosome, considerably higher than for most Icelanders. I found this an interesting and puzzling revelation. To speak of "genealogical dis-ease" (Rapp, Heath, and Taussig 2001) – to use a term developed by anthropologists studying what people make of genetic information about their roots and ancestry – would, however, be an overstatement.

The analysis of mtDNA establishes one's place in a matrilineal family tree spanning 170,000 years. It turned out I belong to "mitogroup R*," a category shared by 4.8 percent of deCODEme users, all of whom can trace their mtDNA to a woman thought to have lived about 60,000 years ago, probably somewhere in the Near East. The analysis of my paternal DNA, on the other hand, showed that I belong to "Y-group R1a," a category shared with 10.3 percent of deCODEme users tracing their Y chromosome back to one man who is thought to have lived about 10,000 to 15,000 years ago, probably in Western Asia.

A further feature allowed users to explore their "map of kinship," a visual representation of genetic space. Given this evidence, I occupy a somewhat marginal position, neither firmly within the European reference group nor any of the others, probably reflecting the puzzling observation mentioned above about my East Asian ancestry. The final feature allowed the user to compare

his or her genome with that of a reference individual from any of the populations included in the data set.

The other main service offered by deCODEme is that of analyzing the genome with respect to specific traits and health risks. For some weeks I resisted the lure of the health results. Both of my parents had struggled with cancer, and I was not that interested in the kind of fortune telling offered by personal genomics. I guess news of the New York spit party helped to change my mind. Somehow, collective spitting appealed to the anthropologist curious about the social life of DNA and the implications of the new genetics in the modern age. My results for the forty-seven diseases and traits covered at the time were based on calculations comparing my genome to sequences of participants in studies published in the scholarly literature. To access results for some diseases, I was invited to read about the genetic and medical details and to sign a statement about informed consent by clicking on "Accept." I need not bore the reader with the personal details. Suffice it to say that some of the information provided sounded trivial (no alcohol flush reaction), some of it resonated with what I thought I already knew (I am less likely than the general population "to become nicotine dependent [15 percent or less]"), some results were encouraging (I have low lifetime risk of some diseases, much less than for males of European ancestry in general), and some details might promote the hypochondriac in me to request further medical information (my risks for some diseases are slightly higher than those of my genetically significant others). When presented with these results, I was offered details on the mathematics of risk analysis. Also, I was invited to zoom in on my genomic landscape, focusing on a part of a chromosome and the location of specific mutations reportedly responsible for potential traits or diseases. Again, there were some surprises and some food for thought.

The Genome Browser of deCODEme allowed users to compare their complete data with friends and family. While my reference group of friends and family included both hypochondriacs and anthropologists, they had seen few good reasons to participate and, as a result, there was not much to compare. The website, however, allowed me to examine my genetic sharing with "famous" people. Here, sharing was indicated visually by the coloring of the relevant bits of the chromosomes. No doubt personal genomics is becoming both a family affair and a global concern. At any rate, a thriving imagined community of the users of personal genomics projects has been developing on the Internet.

2.4 Cyberspace: the experts and the rest

A number of websites testify to a lively discourse on the issues involved, including thinkgene.com, dna-forums.org, Eye on DNA, Urban Semiotics,

and Dienekes' Anthropology Blog. The last one is dedicated to human population genetics, physical anthropology, archaeology, and history. Judging from these websites, there is more interest in exploring ancestry than health risks. Perhaps users are reluctant to reveal their health risks in public, although they may be keen to download the relevant information for their own purposes. Some of the websites referred to are focused on specific personal genomics projects while others are more general. Users engage with the goals of personal genomics, analyses of their own genome, and comments expressed through the expanding virtual community of the Internet.

Often, users comment on each other's roots and genetic identification, usually identifying themselves by first names or nicknames. In World Families Forum (2008), one user offered the following statement, referring to one of Sykes's seven daughters of Eve, Ursula: "Both my wife and I are U5a1a (Clan Ursula) members and on my Y side I am an R1b1c. We believe we are part of the Vandals, Visigoths, and the Normans groups of people who settled in Sicily – who were ancient Vikings/Scandinavians." Another user responded: "Some information about your R1b1c ... It is unlikely that it is of Viking descent. More likely it originated in western Russia." In some cases, users deliberately request advice or interpretation: "This is a nice website and I have enjoyed it. I have recently had my mtDNA tested and have been identified as a U5 (weak match). Can anyone please tell me what the 'weak match' means? I thought a match was a match. Thanks bunches!!"

Clearly, this is a biosocial community in the making, social networks based on identification with genomic characteristics. A certain "countess" commented, "I just found out that I am a daughter of Ulrike. Wow, how amazing to feel this connection to the past ... My ancestry is almost all British Isles, but I didn't know we were descended from Vikings!" (Family DNA 2008b). Another user, "PDHOTLEN," reported after "psyching" himself or herself to have the results of a mtDNA test: "My results (U5) say that my maternal ancestors were responsible for the demise of the Neanderthals in Europe ... Does anyone out there have a similar mtDNA?" Soon there was a response: "I also have U5, but my ancestors were probably not among the cave decorating Cro-Magnons. They are the Saami people up in the northwestern corner of Europe ... Getting the results from the genetic tests has made me a hobby genealogist and with good helpers I have been able to trace some Saami relatives back to the beginning of 1600" (Family Tree DNA 2008).

While many users become knowledgeable and skillful readers of genomic texts in the process of blogging, sometimes the technical jargon becomes overpowering, reaffirming the dividing line between experts and laypersons. Consider the following exchange.

DIDIER: The problem with the shorthand naming is that you lose contact with the subgrouping. Only those familiar with R1b haplogroups would know that R-U106 is distinct of RU152, R-SRY2627, R-L21 . . . I would favor a simplified nomenclature . . . The others are cryptic, very interesting for the specialist (those of us discussing these issues are specialists) but very confusing for non-specialists.

BANKS: It appears to me that you specialists will be preaching to the choir because the congregation (non-specialists) will be long lost in a state of utter confusion . . . I have no knowledge of the "longhand" let alone the shorthand of DNA classifications. I only recently learned to spell haplotype. (World Families Forum 2008)

Occasionally, renowned experts drop in to offer a point of view or to clarify some issue. At one point it seems that James D. Watson, who shared a Nobel Prize for unraveling the structure of DNA, entered the scene, to underline the reliability of the testing provided by personal genomics: "It is important to note that no one is questioning the accuracy of the actual sequencing behind these services"; immediately, there was a respectful response from "docduke": "If that last post was by James D. Watson, I would like to take this opportunity (if you check back), to thank you for your candid, and honest, statements here as elsewhere. Intellectual honesty is becoming altogether too rare in public scientific discussions these days!" (Chron.Com 2008).

Quite possibly, the name "docduke" suggests that the blogger's point in referring to "candid, and honest, statements" is primarily to show support implicitly of Watson's statement in the *Times* of London about race, genetics, and the intelligence of many Africans: "All our social policies are based on the fact that their intelligence is the same as ours – whereas all the testing says not really." Because Watson's own genome is online, his ancestry is open for scrutiny. Exploring the data, the deCODE team concluded, with a hint of irony, that whatever Watson might think of black Africans, 16 percent of his own genes probably come from black ancestors (ABC News 2009).

Some bloggers take a playful attitude to genome testing. One woman who had her husband "tested" for fun was questioned about her ethics.

MEGAN: I admit it. I have no self-discipline when it comes to genetic genealogy. When deCODEme was launched, I had to be one of the first in line to get tested. So I ordered . . . and received results . . . my husband's results, that is. I thought this might be a little more interesting since he sports a Y chromosome.

MARIE: Did you get your husband's permission before using his DNA? . . . How does he feel about you sharing his results with the world?

MEGAN: Yes, rest assured, I checked with him several times just to be sure. (RootsTelevision 2008)

Sometimes people check whether they are being cheated by genomic services. One blogger claimed to know of "at least one case ... where a customer deliberately submitted a dog's DNA just to 'test' the company. He was willing to pay for his little experiment, and yes, the company figured out exactly what had happened!" (RootsTelevision 2008). Sometimes users subscribe to two or more services to compare their usefulness and explore their methods and reliability.

I tested for both 23andMe and deCODEme. I just received my 23andMe results and I am quite surprised by the admixture test named Ancestry Painting. Indeed, I am half Berber, half French (E3b1b-M81, MtDnapI) but my 23andMe results showed 100% European (African and Asian p 0%) whereas my deCODEme results showed 81% European, 13% African ancestry and 6% Asian ... Do you know if these very different results can be because of different method used between 23andMe and deCODEme? (Dienekes' Anthropology 2008)

Concerned more with estimates of health risks than ancestry, Francis Collins, director of the US National Institutes of Health, caused a stir in 2009 by announcing that he had signed up for several personal genomics services under a false name, comparing and testing their prognoses. While sequence-wise, he concluded, the tests appeared to be "highly accurate," the final risk score varied from case to case: "[O]ne company used 5 single nucleotide polymorphisms, or SNPs, to calculate risk for a particular disease, pronouncing Collins at low risk. Another used 10 SNPs, placing him at high risk, and the third used 15, concluding that he is at average risk" (ScienceBlogs 2009).

It seems that the virtual community of genetic citizens is actively debating and negotiating roots, identities, and health risks by fusing the expertise of geneticists and nonprofessionals for the purpose of scrutinizing SNPs and comparing haplotypes. To some extent, however, the experts and the public engage in separate conversations. Nevertheless, representing just a tip of a rapidly expanding iceberg, the preceding excerpts from the Internet give some idea of the discursive community involved, the relations established, and the concerns people have.

2.5 From genome to identity

In some of his last writings, Foucault (1988) shifted his attention from systems of domination to the agency and experience of the individual, drawing attention to the particular kind of subjectivity characteristic for the modern age and what he called "technologies of the self." It seems reasonable to argue that personal genomics represent one example of technologies of the self

(Hacking 2006). Indeed, the genomics of ancestry is often assumed to provide an important avenue into identity and personhood. Significantly, Sykes's (2001) book on ancestry, which opens with the question "Where do I come from?," closes with a chapter titled "A Sense of Self." Anne Wojcicki, the cofounder of 23andMe, also underlines this point; the 600,000 genetic markers interpreted by 23andMe, she argues, are "the digital manifestation of you" (Hamilton 2008). Knowing where we come from, we apparently also know who we are.

Not only is there a growing popular literature that equates human beings with their genomes, this is also a theme explored in endless blogs on the websites mentioned above. One of the relevant statements suggests, in a somewhat humorous tone, that DNA "speaks" to its host:

> I received my DNA results earlier this year and was surprised to find myself in clan Ulrike. I have traced six generations of maternal ancestors in the Beds/Northants borders region. The Viking invaders did travel into this area . . . I have always been attracted to northern wilderness and have visited Alaska, Greenland/Iceland and Siberia. Is this my DNA speaking?! (Family DNA 2008a)

DNA, then, from the past tends to be seen as an avenue into the future, our essence and fate.

Battaglia (1995: 3) suggests an "approach to selfhood as embodied and historically situated practical knowledge," which in her view "prompts a larger question of rhetoric, namely, what use a particular notion of self has for someone or for some collectivity." Given such an approach, an important theme on the anthropological agenda is to explore the rhetoric of personal genomics and the pragmatic uses of genetic notions of self for the actors involved (see, for example, Gibbon and Novas 2007). Nowadays, with personal genomics, the collection and analysis of DNA are closely linked to commercial marketing of identity, including "race." Anxious to explore the unique signatures of their genomes and to care for their selves and their bodies, people are buying in rather than being solicited or tracked down. In the process, they facilitate the construction of gigantic DNA assemblies, coproducing knowledge of genomic differences.

2.6 Conclusions

As we have seen, there is a rapidly growing interest in personal genomics for the purpose of reconstructing our past and celebrating our emerging biosociality and for managing our lives and our future. Day by day, the companies involved have offered additional services on their websites, further details on diseases and traits, higher resolutions of data, and more powerful machines, diagnostic chips, visual presentations, and interactive features.

Anthropology is implicated in these developments at several levels, contributing to the key data sets employed on human history and variability.

Several personal genomics services provide information on both ancestry and health risks. For consumers, it seems, the former kind of information, the extraction of history from what Zuckerkandl called molecular "semantides" (see Sommer 2008: 506), usually involves a fair amount of playfulness, sometimes with undertones on identity, race, and networking, while the latter is inevitably associated with serious issues relating to medicine and lifestyle. Explorations of ancestry and health risks, however, overlap, enmeshing users in new biosocial relations and networks. One may wonder whether the relative importance of the two kinds of services may not be considerably altered in the future.

There are serious anthropological and philosophical doubts about important issues relating to ancestry, including the shape of the family tree, the validity of the molecular-clock hypothesis, and the sampling of populations (Bolnick *et al.* 2007). Analyses of ancestry in personal genomics services, however, are likely to remain more or less intact, partly because there is not so much at stake and, in any case, it is largely play. Studies of the genomics of diseases, in contrast, are riddled with contests, doubts, and conflict. Most common diseases, it seems, are only minimally explained by genetic factors, and in each case a great number of genes is likely to be involved. Last but not least, there is growing evidence for the importance of epigenetic factors beyond the simple concept of DNA sequence. Prainsack *et al.* express some of the doubts: "Personal-genomics customers are already going through a process of disenchantment: it is increasingly clear how little power SNP-based readouts of a person's 'genotype' offer for predicting future ailments in an individual" (2008: 35).

Given the evidence and the growing public awareness of it, why would people bother to consult their health risks with personal genomics services? It seems unlikely that the narcissistic pleasures involved in the exploration of ancestry and the genetics of health risks are withering away, given the central place of the human body in late modernity. Also, there are immense financial stakes and concerns on the global level for biotechnical and pharmaceutical companies. Moreover, the quality, magnitude, and comprehensiveness of knowledge can only increase with time. The power of computing machinery continues to expand, and cheap complete sequencing is within reach. As a result, one may expect personal genomics projects to expand, realigning experts and consumers, institutions and disciplines, including anthropology.

The narcissistic pleasures of late modernity are reaching new levels that neither Lasch (1979) nor Foucault (1988) could have anticipated. Personal genomics is just one example. Another example, perhaps, is the use of humans as model organisms in biological experimenting, as human cellular

material replaces that of mice and fruit flies, a point emphasized by Rheinberger (2009: 8): "Many experiments are now being carried out with human cells directly … With man becoming, in a sense, a model organism of his own, 'modeling' inevitably takes on the meaning and the form of human modification." One suspects this significant shift will have profound implications for anthropology and its understanding of the species and its variability, although the terrain is just beginning to be explored.

In recent years, the notion of the tree of life – a central notion for Darwin, Linnaeus, and much of biological thought since their time – has been seriously challenged by a strange mix of scholars such as W. Ford Doolittle, Stefan Helmreich, Tim Ingold, Marilyn Strathern, Gilles Deleuze, and Félix Guattari. For one thing, it has been reasoned, the tree of life might turn out to be a net or a rhizome, with endless reconnections rather than treelike bifurcation. While it is possible that theoretical challenges to the tree model and the empirical evidence available only minimally blur the main picture, simply shaking the tree a bit, they raise fundamental questions as to what should count as relatedness. Why, indeed, should we stick with reductionist gene talk? In the current age of biosociality, life has become increasingly disembodied, cultured, informatic, and rewritable.

Just as the history of physical anthropology and the bone collectors of the last century coalesced at a measuring party, the saga of modern biological anthropology and personal genomics coalesces at a spit party. In some respect, the two parties are rather different. Thus, whereas in the former case, research subjects were tracked down for measurements, often in the context of a colonial hierarchy, in the latter case, subjects offer themselves for the project in the hope that they may, in the process, discover and take care of their selves and bodies. This underlines radically different biosocial relations of production. The measuring party and the spit party, however, have one serious flaw in common – namely, the subtext of human variation, "race," and the presumed split between the biological and the social. After all, "biology" and "society" are not separate realities or categories of being. Human variation, including that identified as "race," is a thoroughly relational, biosocial state of affairs, collective history embodied in the habitus. Theodosius Dobzhansky once remarked that "nothing in biology makes sense except in the light of evolution" (Smocovitis 2012: 122). Given the deliberate conflation of the biological and the social in the wake of the new genetics, the human configuring of life itself, and the advancing evidence on epigenetics and developmental systems (Griffiths and Gray 1998), it would be more appropriate, twisting Dobzhansky a bit, to state that nothing in biology makes sense anyway, except in the light of the irreducible unity of the biological and the social.

The big challenge for anthropology now is to realign the biological and the social on new terms in a nonreductionist fashion. We can continue to craft

our professional selves on two different tracks and to practice the study of humans as if it involved the investigation of two radically separated domains, defending the subdisciplinary boundaries as if they were engraved in our subjects, but it would be both ethnocentric and out of time. It is time to rethink the field on the assumption that *Homo sapiens* is an undivided being and that decoding it – to the extent that the language of "decoding" is the appropriate one – requires integrative perspectives that in the absence of a better non-dualistic language resonate with our biosocial natureculture. This will not be easy, but it is the only meaningful way to go.

The image and the report in the *New York Times* regarding the launch of 23andMe draw attention to the role of metaphors. Reporters quickly drew upon a series of related metaphors; the event was described as a "spit party," the message of 23andMe and personal genomics in general, it was argued, was "when in doubt, spit it out," personal medicine was said to be "within spitting distance," and so on. The people of 23andMe now have a blog site called "The Spittoon," drawing its name from an object also called "spitter," a receptacle for spitting into: "Using nothing more than a bit of saliva (Get it? The Spittoon!), the genotyping process we use analyzes more than 580,000 locations in a person's genome" (Spittoon 2009). It is tempting to assume that the spit is becoming one of the key metaphors we live by, informing our speech and our thoughts. Metaphors, however, just like DNA, frequently undergo mutations, recombining available material from everyday language and experience. The notion of the "spitting image," as we have seen, is a case in point.

The spit party seems to nicely capture various aspects of personal genomics and the gene talk on which it is based, the mechanisms of inheritance, the matching or mis-matching disclosed through the sequencing of DNA material, and the establishing of distance and ancestry, both genetic and social. When spitting out one's saliva one is presumed to provide a spitting image of oneself, encoded in DNA. The transparent metaphor has, finally, been elevated above the debates of etymologists. The emphasis, on the other hand, is no longer on spitting *at* someone (usually a gesture of contempt). Rather it is the conviviality of spitting *with* a fellow human being, for the purpose of celebrating biosocial bonds, for founding social networks based on bodily signatures. With a ginger martini.